

STRUCTURE OF AN E. COLI MEMBRANE PROTEIN

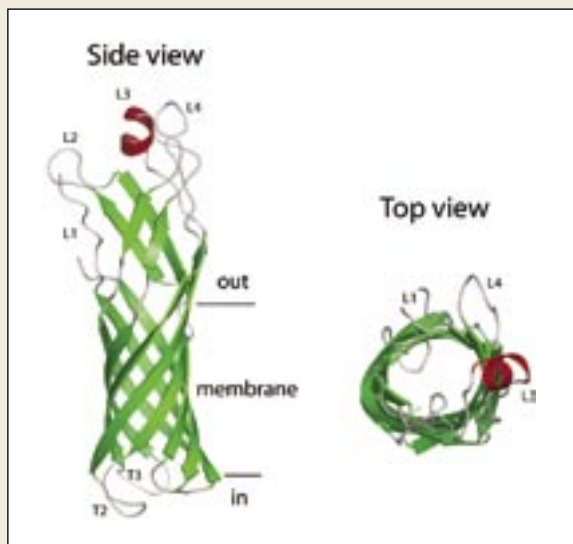
At the NSLS, a team of scientists from the University of Massachusetts Medical School and the University of Virginia have determined the molecular structure of a protein found in the outer membrane of the *E. coli* bacteria. Their work helps to



Cover of the March 17, 2006 edition of the *Journal of Biological Chemistry*

explain how this protein is involved in the overall function of *E. coli* and may one day help in the creation of vaccines against pathogenic *E. coli* strains. The paper was featured as the cover article in the March 17, 2006 edition of the *Journal of Biological Chemistry*.

The protein they studied, known as "OmpW," is a member of a family of small proteins that are situated within the cell membranes of certain bacteria. Membrane proteins have many functions. For example, they are involved in the cell's metabolic processes, provide structural stability, aid in cell-to-cell adhesion, or can protect the cell from outside stresses. Many are also channel-like transport proteins, allowing molecules and ions to enter and exit the cell. However, the lack of good structural data on the OmpW proteins has left scientists uncertain of their particular role.



A side view and top view (from the outside of the cell) of the molecular backbone of OmpW, with the eight strands of the barrel shown in green and the loops (L1 to L4) connecting the strands in grey. The position of the membrane is indicated with horizontal lines.

"Previous crystal structures of proteins related to OmpW suggest that they have channels that are too narrow for them to function as transporters. However, our structure, along with other data, suggests that it can," said Bert van den Berg, a University of Massachusetts Medical School biologist involved in the study. "This helps us understand the role of OmpW with respect to the entire cell."

To obtain the structure, van den Berg and his colleagues worked at NSLS beamlines X25 and X6A. There, they aimed powerful x-ray beams at OmpW protein crystals and observed, using detectors and computers, how the x-rays were diffracted from the atoms in the samples. They then analyzed these diffraction patterns using computer software, which yielded a three-dimensional "snapshot" of the protein's molecular structure.

The structure shows that OmpW is a barrel-shaped protein formed by eight aligned molecular strands. The inside of the barrel forms a long and narrow channel, which is closed on one end. Interestingly, the channel is "hydrophobic," or water-repellent, suggesting that OmpW could form a channel for greasy, hydrophobic molecules.

To learn more about the protein's function, the scientists performed a series of "conductance experiments" on the protein. These tests, which are designed to determine if a membrane protein can form a channel for ions, revealed that OmpW does indeed form a channel. However, which types of ions and molecules are transported by OmpW in the bacterial cell is still unclear.

In future work, van den Berg and his colleagues plan to investigate which greasy molecules, referred to as substrates, are transported by OmpW proteins, and they hope to gain a better understanding as to how the transport process occurs.

For more information, see: H. Hong, D. Patel, L. Tamm, and B. van den Berg, "The Outer Membrane Protein OmpW Forms an Eight-Stranded β -Barrel with a Hydrophobic Channel," *J. Biol. Chem.*, **281**, 7568-7577 (2006).

— Laura Mgrdichian